REMARKS

Claims 1-3, 5, 6, 12-24, and 47 were pending in the present application. Claims 1, 5, 6, 12, 15, 17, 22, and 47 have been amended herein. Claim 20 has been cancelled herein without prejudice to its presentation in another application. No new matter has been added. Upon entry of the present amendment, claims 1-3, 5, 6, 12-24, and 47 will remain pending.

I. The Claimed Invention Is Novel

Claims 17-20 are rejected under 35 U.S.C. §102(b) as allegedly being anticipated by Gillaspy et al., GenEmbl Accession No. U39059 (18 November 1996) (hereinafter, the "Gillaspy reference"). The Office Action asserts that the Gillaspy reference reports a DNA sequence consisting of 60 contiguous nucleotides of SEQ ID NO:1 that are not selected from nucleotides encoding amino acids 70 to 136. Applicants traverse the rejection and respectfully request reconsideration because the Gillaspy reference does not teach every feature recited in claims 17-20.

A sequence alignment of the Gillaspy sequence and SEQ ID NO:1 shows only that the two sequences possess 52 contiguous adenosines in common in the poly A tail and 8 other bases in common. The Gillaspy sequence, however, **does not** represent a nucleic acid **probe** because it has only limited GC content and does not appear likely to act as a probe at a reasonable stringency. Further, one skilled in the art would be very unlikely to select a probe that contains a sequence that is quite clearly not in any way specific to a particular sequence. Thus, although the Gillaspy sequence is a DNA sequence, it does not amount to a probe.

The Office Action continues to assert that Applicants are arguing features (i.e., ability to hybridize to a specific target sequence under conditions of specified stringency and specificity) that are not recited in the claim. To the contrary, Applicants are not reciting "a nucleic acid molecule" in the claim; rather, Applicants recite a "probe" in the claim. The term "probe" actually means something to one skilled in the art and is distinguishable as a subtype of a nucleic acid molecule. Probes have inherent features such as those discussed above which render them useful as probes. Indeed, one skilled in the art would be very unlikely to select a probe that contains a 52-base polyA sequence that would quite clearly not be specific to a plant DP

sequence, let alone any other sequence. Indeed, such a "probe" alleged in the Office Action to be taught by the Gillaspy reference would not function as a probe for anything -- it would be expected to hybridize non-specifically to many molecules. Thus, although the Gillaspy reference reports a nucleic acid molecule, **the nucleic acid molecule is not a probe**.

Thus, the Gillaspy reference does not teach every feature recited in claims 17-20. Accordingly, Applicants respectfully request that the rejection under 35 U.S.C. §102(b) be withdrawn.

II. The Claimed Invention Is Useful

Claims 1-3, 5, 6, 12-24, and 47 are rejected under 35 U.S.C. §101 as allegedly failing to be supported by either a specific, substantial, or a well-established utility. Claims 1-3, 5, 6, 12-24, and 47 are also rejected under 35 U.S.C. §112 as because one skilled in the art would allegedly not know how to use the claimed invention. The Office Action continues to assert that Applicants have not established a specific use for the claimed DNA sequences, and thus, the claimed DNA sequences have no real-world use. Applicants traverse the rejection and respectfully request reconsideration thereof because the claims are supported by specific, substantial, and credible utilities, and thus one skilled in the art would know how to use the claimed invention.

The Office Action continues to assert that the combination of sequence similarity and functional evidence in Applicants' specification does not establish a specific and substantial utility for the protein comprising SEQ ID NO:2. To the contrary, the protein comprising SEQ ID NO:2 is a previously undescribed member of the E2F dimerization partner (DP) proteins. This activity **has been established** through a combination of **sequence similarity** and **functional evidence** as presented in the application, for example, in Examples 1, 5, 6, 7, and 9 and Figures 2 and 3.

The Final Rejection asserts that partial homology between SEQ ID NO:2 and a protein of unknown function (referring to Figure 3) does not impute functional characteristics to SEQ ID NO:2. Applicants' specification, however, provides ample sequence similarity data to indicate

that the protein comprising SEQ ID NO:2 is a plant DP protein. For instance, Example 1 in Applicants' specification teaches:

> An amino acid homology study using the CLUSTALW routine (carried out on July 25,1999) with the available sequences of DP proteins from animal origin was carried out (Figure 2). **Alignment of the TmDP with the animal DP sequences available in public databases revealed the existence of several conserved motifs, strongly suggesting that the TmDPcDNA clone encodes a protein belonging to the family. This together with its ability to interact with a plant E2F protein, indicates that the TmDPcDNA encodes a bona-fide plant DP protein**. (emphasis added).

In addition, Example 9 in Applicants' specification teaches:

> Characterisation of TmDP
>
> **The idea that the isolated CDNA encodes a plant member of the DP family was reinforced by analysis of the amino acid homology and domain organization.**
>
> TmDP exhibits an overall 29-33% amino acid similarity with human (Bandara et al., 1993; Girling et al., 1993; Krek et al., 1993) and X. laevis (Girling et al., 1994) DP-1 and DP-2 and a slightly smaller similarity (27%) with D. melanogaster DP (Dynlacht et al., 1994; Ohtani and Nevins, 1994). Amino acid alignment of plant and animal DP proteins indicates that it has a similar domain organization (Fig. 3B). The highest homology occurs within a 70 amino acid region (residues 64-143 in TmDP) which in animal DP proteins are important for DNA binding (Wu et al., 1996). This region includes a 10 amino acid stretch of fully conserved residues. Other amino acid blocks with a significant degree of homology contain the heptad repeats (residues 144-213 in TmDP), involved in heterodimerization with E2F (Wu et al., 1996; Zheng et al., 1999) and the domain conserved with E2F proteins (residues 214-240 in TmDP), a region which is similar to the E2F family members (Girling et al.,1993).
>
> Experimental evidences of the heterodimerization properties of TmDP will be presented below in detail. Quite interestingly, TmDP lacks an acidic region which is present near the C-terminus of animal DP members, a domain whose functional significance has not been determined. Finally, the less conserved region corresponds to the N-terminal domain whose length and amino acid sequence is similar to that of animal DP members, in particular to the DP-2 group. **Based on these**

> **homology studies, we conclude that TmDP presents a higher amino acid sequence similarity to animal DP-2.** However, it is worth noting its smaller size and the absence of an acidic C-terminal domain as unique properties of TmDP.

Thus, quite clearly, Applicants' studies of sequence data indicates that the protein comprising SEQ ID NO:2 is a plant DP protein.

The functional data presented in Applicants' specification also indicate that the protein comprising SEQ ID NO:2 is a plant DP protein. E2F transcription factor is a protein known to be involved in the transition of G1/S phases in the plant cell cycle. Typical DP proteins form stable heterodimers with E2F family members and can promote binding of E2F to DNA. The protein comprising SEQ ID NO:2 binds to and modulates the binding to DNA of the plant E2F transcription factor (see Examples 5-7).

If the Examiner is aware of any *evidence* that would teach that a protein comprising SEQ ID NO:2 is NOT a DP protein, then Applicants respectfully request that such evidence be brought to light. Otherwise, in the absence of such evidence, the Patent Office must take Applicants assertions as true.

The Office Action asserts that the binding of the protein comprising SEQ ID NO:2 to an E2F transcription factor protein and its stimulation of E2F binding to DNA does not establish a specific and substantial utility because it is not apparent how these properties have a real world use. It is not the properties per se, however, that provide the "real world use" of the protein. The combination of the sequence similarity data and the functional studies quite clearly establish that the protein comprising SEQ ID NO:2 is a plant DP protein. Plant DP proteins have quite many real world uses. Indeed, the description at page 4, line 14 to page 5, line 10 provides specific, substantial, and credible uses for modulation of these activities. Furthermore, these specific, substantial, and credible uses are supported by the teaching of PCT Publication WO0047614 (applicant Pioneer) which discusses even more specific, substantial, and credible uses for plants with modified expression of the DP proteins. Further, Applicants discuss numerous "real world" uses for DP proteins at, for example, pages 3 to 5 of the specification.

WO 00/47614, for example, teaches real world uses for DP proteins. Because the protein comprising SEQ ID NO:2 has been quite clearly established as a plant DP protein, and

plant DP proteins have known specific, substantial, and credible utilities, the protein comprising SEQ ID NO:2 has at least one specific, substantial, and credible utility. Furthermore, DNA encoding such a protein also has at least one specific, substantial, and credible utility.

Thus, the claimed DNA clearly has a useful, concrete and tangible use and, thus, is patentable subject matter. Accordingly, Applicants respectfully request that the rejection under 35 U.S.C. §101/§112 be withdrawn.

III. The Claims Are Clear And Definite

Claims 1, 5, 6, and 12 are rejected under 35 U.S.C. §112, second paragraph, as allegedly being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicants regard as their invention. Although Applicants believe the claims are clear and definite as originally drafted, solely to advance prosecution of the present application, Applicants have amended claims 1, 5, 6, and 12 to be even more clear and definite. No new matter has been added.

A. Claim 1

The Office Action asserts that claim 1 is indefinite in recitation of "controlling." Claim 1 recites a "method of controlling one or more of plant growth, gene expression, cellular DNA replication, cell cycle progression, differentiation and development…" Although Applicants disagree with the reasoning set forth in the Office Action, solely to advance prosecution of the present application, claim 1 has been amended to replace "controlling" with "increasing."

The Office Action also asserts that the phrase "increase or decrease" in claim 1 is unclear. Although Applicants maintain that the phrase is as clear as can be, solely to advance prosecution of the present application, claim 1 has been amended to recite "increase." Accordingly, claim 1 is definite within the meaning of §112. *In re Mercier*, 185 U.S.P.Q. 774 (C.C.P.A. 1975) (claims sufficiently define an invention so long as one skilled in the art can determine what subject matter is or is not within the scope of the claims).

B. Claim 5

The Office Action asserts that the phrases "altering", "modulation", and "increasing or decreasing" are indefinite. Although Applicants disagree with the reasoning set forth in the Office Action, solely to advance prosecution of the present application, claim 5 has been amended to recite "increasing" in all three places.

C. Claim 6

The Office Action asserts that the phrases "modification", "activity", and "increased or decreased" are indefinite. Although Applicants disagree with the reasoning set forth in the Office Action, solely to advance prosecution of the present application, claim 6 has been amended to recite "an increase", "DP/E2F dimerization", and "increased" respectively.

D. Claim 12

The Office Action asserts that the phrase "modulation" is indefinite. Although Applicants disagree with the reasoning set forth in the Office Action, solely to advance prosecution of the present application, claim 12 has been amended to recite "increasing."

In view of the foregoing, the claims are clear and definite. Accordingly, Applicants respectfully request that the rejection under 35 U.S.C. §112, second paragraph be withdrawn.

IV. The Claimed Invention Is Supported by Ample Written Description

Claims 1-3, 5, 6, 12, 13, 15, 22-24, and 47 are rejected under 35 U.S.C. §112, first paragraph, as allegedly containing subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. Applicants traverse the rejection and respectfully request reconsideration because the specification provides ample written description supporting the claimed inventions.

As stated in the "Guidelines for Examination of Patent Applications Under the 35 U.S.C. Sec. 112, para. 1 'Written Description' Requirement,":

> Possession may be shown by actual reduction to practice, by a clear depiction of the invention in detailed drawings which permit a person skilled in the art to clearly recognize that applicant had possession of the claimed invention, or by a written description of the invention describing sufficient relevant identifying characteristics such that a person skilled in the art would recognize that the inventor had possession of the claimed invention.

In accordance with these standards, Applicants have indeed, provided a sufficient written description of the claimed inventions. For example, claim 1 recites that a plant cell is transformed with a nucleic acid comprising ***a sequence encoding SEQ ID NO:2, or a functional part thereof, or a sequence having at least 70% homology***. These features alone are sufficient to establish that Applicants were in possession of the claimed invention. A description of a specific percent homology also provides an adequate written description. Claim 1, for example, also recites that the peptide or protein dimerizes with a plant E2F protein or peptide to increase E2F activity in the plant cell. Claim 1 further recites that the protein or peptide comprises at least one of the following structural features: a) the DNA binding domain, b) the heterodimerization domain, and c) the nuclear localization signal (i.e., a functional part thereof). These features are common to DP proteins, as outlined in Figure 2, and as described on page 12, lines 3-7, and as such are a recitation of features common to members of the genus, which features constitute a substantial portion of the genus. Thus, claims recite a proper combination of structure and function.

The Office Action continues to assert that recitation of structure and function in the claim does not describe the claimed invention because the recited genus has not been described. In particular, the Office Action continues to assert that the one example provided in Applicants' specification does not constitute a representative number of species. The Office Action continues to focus only on a representative number of species, when a representative number of species is but one of many ways of demonstrating possession. Indeed, as explained in the previous paragraph, Applicants have demonstrated possession of the claimed invention by recitation of a sequence (SEQ ID NO:2) in combination with functional activity. Even if the Office Action continues to focus only on a representative number of species, there are situations where a single

specifically disclosed species is adequately supports a genus. For example, the MPEP §2163 states:

> Satisfactory disclosure of a "representative number" depends on whether one of skill in the art would recognize that the applicant was in possession of the necessary common attributes or features of the elements possessed by the members of the genus in view of the species disclosed.

The structural, homology, and functional features recited in Claim 1, for example, demonstrate Applicants were in possession of the necessary common attributes or features of the elements possessed by the members of the genus in view of the species disclosed. Additional species are not warranted in the present situation because Applicants recite common attributes or features of the elements possessed by the members of the genus in view of the species disclosed. Further, the requirements of §112, first paragraph, regarding written description are met so long as the invention is described in the specification as broadly as it is claimed. *In re Marzocchi*, 169 U.S.P.Q. 367 (C.C.P.A. 1971).

In view of the foregoing, Applicants respectfully request that the rejection under 35 U.S.C. §112, first paragraph, as allegedly failing to provide sufficient written description be withdrawn.

V. The Claimed Invention Is Sufficiently Enabled

Claims 1-3, 5, 6, 12, 13, 15-24, and 47 are rejected under 35 U.S.C. §112, first paragraph as allegedly failing to provide an enabling disclosure. The Office Action mistakenly asserts that the asserted uses are not enabled because the specification does not provide sufficient guidance with respect to: 1) "how to use any protein expressed from any of the claimed sequences"; 2) "how to use any of the claimed sequences to detect any particular nucleic acid sequences"; or 3) "how to use any of the claimed sequences to amplify any particular DNA fragment." Applicants traverse the rejection and respectfully request reconsideration because one skilled in the art would be able to practice the claimed invention without being required to perform undue experimentation.

A. Claims 1-3, 5, and 6

As a preliminary matter, Applicants have provided a specification that enables one skilled in the art to make and use the ***claimed invention*** without being required to perform undue experimentation. In this regard, claim 1 recites a method of increasing one or more of plant growth, gene expression, cellular DNA replication, cell cycle progression, differentiation and development in a plant cell by transforming the plant cell with a nucleic acid. The nucleic acid comprises a nucleotide sequence that encodes a peptide or protein that comprises SEQ ID NO:2, or a functional part thereof, or a sequence having at least 70% homology to either. The peptide or protein also dimerizes with a plant E2F protein or peptide to increase E2F activity in the plant cell. Also, E2F activity is E2F binding to E2F binding sites in plant DNA. Further, the peptide or protein comprises a) a DNA binding domain, b) a heterodimerization domain, and c) a nuclear localization signal. Claims 2, 3, 5, and 6 are dependent on claim 1.

The Office Action appears to assert that one skilled in the art must perform undue experimentation to carry out the claimed method. The Office Action, however, appears to accept the fact that one skilled in the art can make the nucleic acid molecules and transform plant cells with them without being required to perform undue experimentation. The Office Action asserts that the rejection was predicated on Applicants' alleged failure to provide specific guidance with respect to which sequences to make and test, and with respect to which functional assays to apply to which sequences in order to discriminate between those sequences that function as desired and those that do not. Applicants disagree.

One skilled in the art would, based on Applicants' specification, be able to make any nucleic acid that: 1) encodes a peptide or protein that comprises SEQ ID NO:2, or a functional part thereof, or a sequence having at least 70% homology to either; 2) dimerizes with a plant E2F protein or peptide to increase E2F activity in the plant cell; 3) where E2F activity is E2F binding to E2F binding sites in plant DNA; and 4) wherein the peptide or protein comprises a DNA binding domain, a heterodimerization domain, and a nuclear localization signal. The specification teaches the function of these domains (see, for example, page 19, line 22 to page 21, line 16) and they are demonstrated to be present in other DP proteins. The specification teaches ample methods of verifying the activity of the proteins (see, for example, those of

Examples 2, 4, 6, and 7). Therefore, there is no amount of experimentation identified in the Office Action that would be undue in order to practice the claimed invention. Indeed, one skilled in the art would be able to make any nucleic acid having the elements recited in the claims without undue experimentation. Further, one skilled in the art would be able to test individual nucleic acid molecules in the assays described in Applicants' specification to determine their particular activity (whether it increases, or decreases in the case of antisense) without undue experimentation -- even voluminous research is not undue so long as it is of a routine nature. *Ex parte Forman*, 230 U.S.P.Q. 546, 547 (Pat. Off. Bd. App. 1986). Significantly, the Office Action does not specifically point out which particular aspect requires undue experimentation.

The Office Action dated March 15, 2005 asserts that the invention is not enabled because "the effect of expressing in a cell a DP protein, alone or in combination with an E2F protein, is unpredictable, since different members of both the DP protein family and the E2F protein family vary with respect to their specific functions, and with respect to how they function when expressed independently and when coexpressed." The present Office Action appears to take the same position. Applicants disagree. The Office Action cites six references which purportedly supports the Examiner's position, only two of which relate to plant DP proteins.

The fact that DP proteins may have many different functions, ***particularly in non-plant cells***, is wholly irrelevant in determining whether one skilled in the art can practice the claimed invention in ***plant*** cells without being required to perform undue experimentation. The various functions of DP proteins reported in the Hiebert, Dynlacht, Sawado, and Wu references are directed to ***non-plant cells***. Applicants are unable to locate any portion of these references that teaches or suggests that the observations of different proteins in a different kingdom are what would also be expected in plants. Whether or not these functions are "predictable" is irrelevant when determining whether undue experimentation is required to carry out the claimed method in ***plant*** cells. Despite the statements in the current Office Action, Applicants comments with respect to these references still stand.

Magyar et al., FEBS Lett., 2000, 486, 79-87 (hereinafter, the "Magyar reference) does not teach or suggest that Applicants' claimed invention does not work or would require undue experimentation to work. Rather, as acknowledged in the Office Action dated March 15, 2005,

the Magyar reference merely reports that *Arabidopsis thaliana* DP proteins do not group with animal DP families. Applicants are unable to understand any significance or relationship this plays in regard to Applicants' claimed invention. Again, nowhere does the Magyar reference teach or suggest that, because of the differences between *Arabidopsis thaliana* DP proteins and animal DP proteins, Applicants' claimed invention (which makes use of wheat DP proteins) would not function in plants, or would require undue experimentation to work in plants.

Mariconti et al., J. Biol. Chem., 2002, 277, 9911-9919 (hereinafter, the "Mariconti reference) also does not teach or suggest that Applicants' claimed invention does not work or would require undue experimentation to work. Rather, the Mariconti reference reports the existence of another group of E2F proteins in *Arabidopsis thaliana* which appear to lack the ability to bind to DP proteins, **in addition** to the group of E2F proteins that can bind to DP proteins. The Mariconti reference speculates that this additional group of E2F proteins can compete with the "wild-type" E2F proteins. Again, Applicants are unable to understand any significance or relationship this plays in regard to Applicants' claimed invention. Nowhere does the Mariconti reference teach or suggest that, because of the existence of another group of E2F proteins in *Arabidopsis thaliana*, Applicants' claimed invention (which makes use of wheat DP proteins) would not function in plants, or would require undue experimentation to work in plants. The Mariconti reference does not teach or suggest that Applicants' claimed methods would not work in plant cells that also express such additional group of E2F proteins.

The Office Action also asserts that the invention is not enabled because methods for inhibiting the expression of endogenous genes using antisense technology are unpredictable, since the ability of an antisense DNA sequence to inhibit gene expression is dependent on the specific structure of the DNA sequence and its target. The Office Action cites three references which purportedly supports the Examiner's position. Applicants again disagree.

None of the references teach or suggest that any amount of undue experimentation must be performed to practice the claimed invention. Rather, the three references report that some antisense compounds are better than others and that a high degree of sequence homology (i.e., greater than 75%) between the endogenous gene and the antisense compound is required in order for the antisense compound to be effective. The fact that some antisense compounds work better

than others is not surprising, let alone sufficient to establish that undue experimentation is required to practice Applicants' claimed invention. In addition, the fact that a high degree of complementarity is also involved is also wholly unsurprising. It does not take any amount of undue experimentation to design an antisense compound with a sufficient degree of complementarity so as to effectuate hybridization. The general principals of the construction of antisense sequences and how to express them in plants is broadly appreciated in the art. Further reference is made to U.S. Patent No. 5,107,065 (cited in the current application and included therein by reference – see page 15, lines 20-27 of the specification) which teaches general principals of the construction of antisense compounds. These are reduced to practice by simple matching to the disclosed sequence. There is no undue burden on the ordinarily skilled artisan given the level of skill in this area and the availability of modern screening practices.

Thus, there is no reason to believe that one skilled in the art would be required to perform any amount of undue experimentation to make and use the claimed invention. Accordingly, Applicants respectfully request that the rejection under 35 U.S.C. §112, first paragraph be withdrawn.

B. Claims 12, 13, 15-24, and 47

As a preliminary matter, claims 12, 13, 15-24, and 47 recite an "isolated, enriched, cell free and/or recombinant nucleic acid" (claims 12 and 13), a "nucleic acid probe" (claims 16 and 17), an "oligonucleotide probe" (claims 18 and 19), a "DNA which is antisense" (claim 21), a "nucleic acid" (claims 22 and 23), a "nucleic acid vector or construct" (claim 24), and a "nucleic acid encoding a DP peptide or protein fused to a sequence encoding a protein label" (claim 47). Thus, each of these claims recites compounds rather than methods of using compounds. No amount of undue experimentation is required to make or use any of the claimed compounds. Indeed, nucleic acid compounds are routinely made and used by those skilled in the art.

Applicants remind the Examiner that any use of the compounds recited in these claims is sufficient for purposes of enablement. For example, the claimed nucleic acid compounds can be used, for example, to either express a DP protein having SEQ ID NO:1, to detect nucleic acid sequences encoding a protein having SEQ ID NO:1, or can be used as a primer for amplifying a

sequence encoding SEQ ID NO:1 (see, page 12, line 13 to page 16, line 12 of the specification). No amount of undue experimentation is required to use any of the claimed compounds, for example, to express a DP protein having SEQ ID NO:1, to detect nucleic acid sequences encoding a protein having SEQ ID NO:1, or as a primer for amplifying a sequence encoding SEQ ID NO:1.

The Office Action asserts that the rejection was predicated on Applicants' alleged failure to provide guidance on which specific nucleotide sequences to use as probes, the conditions for their use, and the specific targets that can be detected. The Office Action further asserts that such guidance is necessary because Gillespie, Vet. Microbiol., 1990, 24, 217-233 (hereinafter, the "Gillespie reference") purportedly sets forth that the conditions for using a sequence as a probe are unpredictable. Absent such guidance, the Office Action asserts that one skilled in the art would have to make the compounds and test them to determine which probe sequences are useful. Applicants disagree.

As set forth in the Office Action dated March 15, 2005, the Gillespie reference reports that specific hybridization between a DNA probe and its target sequence are affected by: 1) the concentration of probe and target molecules, 2) the length and sequence of the probe, 3) the hybridization temperature, and 4) the concentration of the salt and detergent present during hybridization. The fact that hybridization of a DNA probe to a target molecule is "affected" by any or all of these factors is wholly unsurprising. Indeed, these factors are simply the laws of physics that apply to hybridization of one entity to another entity. These factors, however, in no way, shape, or form amount to undue experimentation. Indeed, the use of DNA probes was routine in the art at the time of the Gillespie reference (1990), let alone as of 1999 (Applicants' earliest priority date). The literature is replete with references describing the use of DNA probes to nucleic acid molecules. Indeed, the general principles involved in the selection of DNA sequences for use as a probes is part of the common general knowledge of the ordinarily skilled molecular biologist. Further, it is routine practice in the art to optimize detection by varying temperature and salt concentration until satisfactory detection is achieved, and/or, if necessary, to use a selection of probes derived from the sequence. Since the sequence of SEQ NO:1, from which the probe sequence must be derived, is defined, the selection of probes does not involve

examination of a myriad of possibilities, but is limited by the sequence from which the probe is derived (SEQ ID NO:1) and the selection of those areas of the sequence with the appropriate physical properties for use as a probe. These properties are well known in the art, consequently this does not represent an undue burden but is simply routine practice in the art to which the application relates.

In sum, no amount of undue experimentation is required to make any of the nucleic acid molecules within the scope of the claims. In addition, there is no amount of undue experimentation to use the nucleic acid molecules to express the DP protein or peptide, or to use them as probes or primers. That one skilled in the art may have to perform some experimentation to determine which nucleic acid molecules work the best does not mean that the claims are not enabled. Indeed, any testing that may be desirable by on skilled in the art is disclosed in Applicants' examples.

In view of the forgoing, one skilled in the art would not be required to perform any amount of undue experimentation to make and use the compounds recited in claims 12, 13, 15-24, and 47. Accordingly, Applicants respectfully request that the rejection under 35 U.S.C. §112, first paragraph be withdrawn.

VI. Conclusion

In view of the foregoing, Applicants respectfully submit that the claims are in condition for allowance. An early notice of the same is earnestly solicited. The Examiner is invited to contact Applicants' undersigned representative at (215) 665-6914 if there are any questions regarding Applicants' claimed invention.

Respectfully submitted,

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